

Supplemental Figures

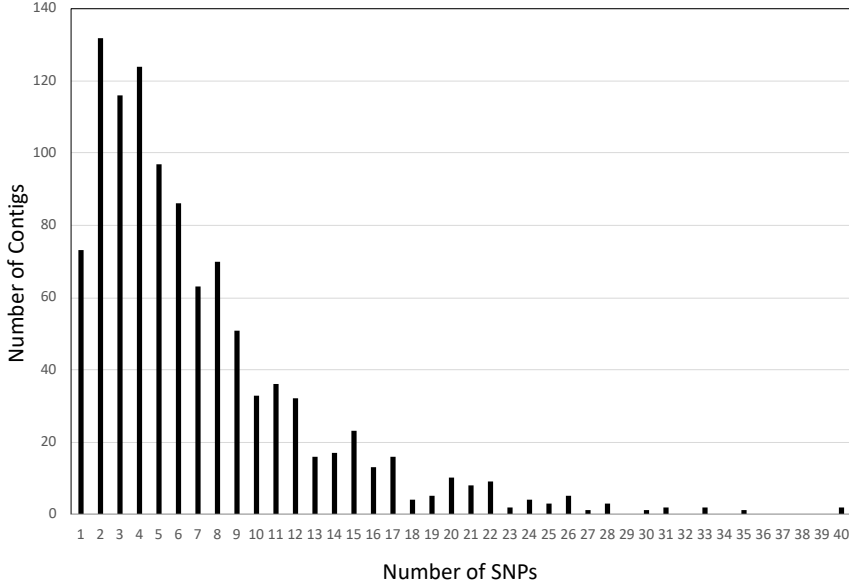


Figure S1. Distribution of SNPs per contig.

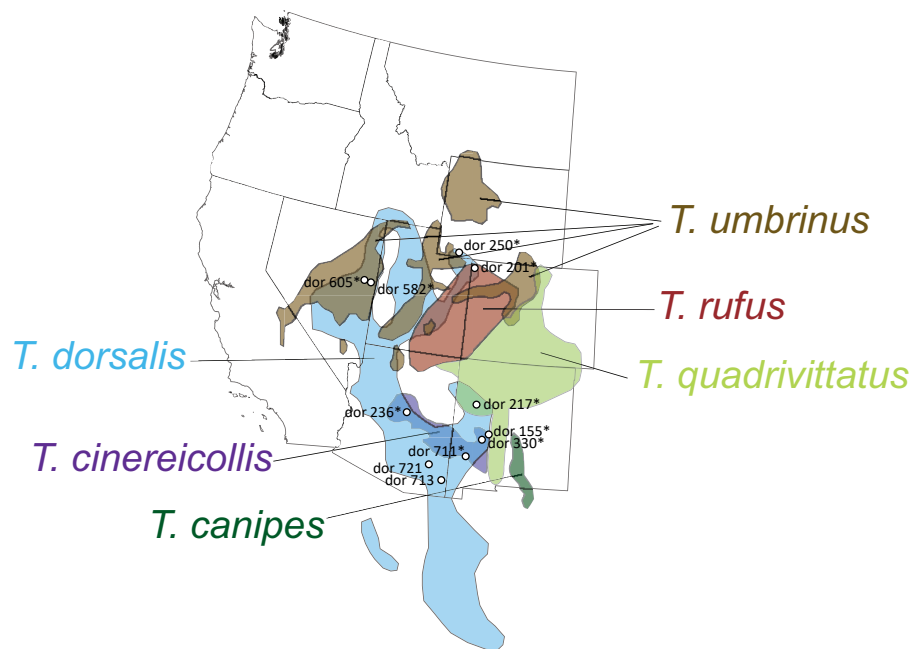


Figure S2. Distribution of *T. dorsalis* individuals sequenced here. Georeferenced localities are presented in Table S2. Individuals inferred to have introgressed mtDNA genomes are denoted by asterisks.

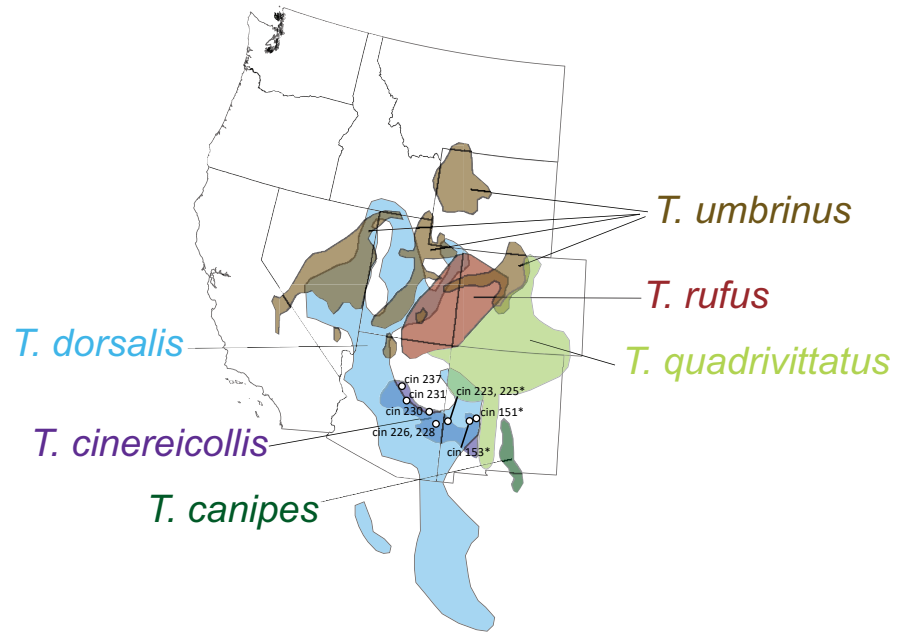


Figure S3. Distribution of *T. cinereicollis* individuals sequenced here. Georeferenced localities are presented in Table S2. Individuals inferred to have introgressed mtDNA genomes are denoted by asterisks.

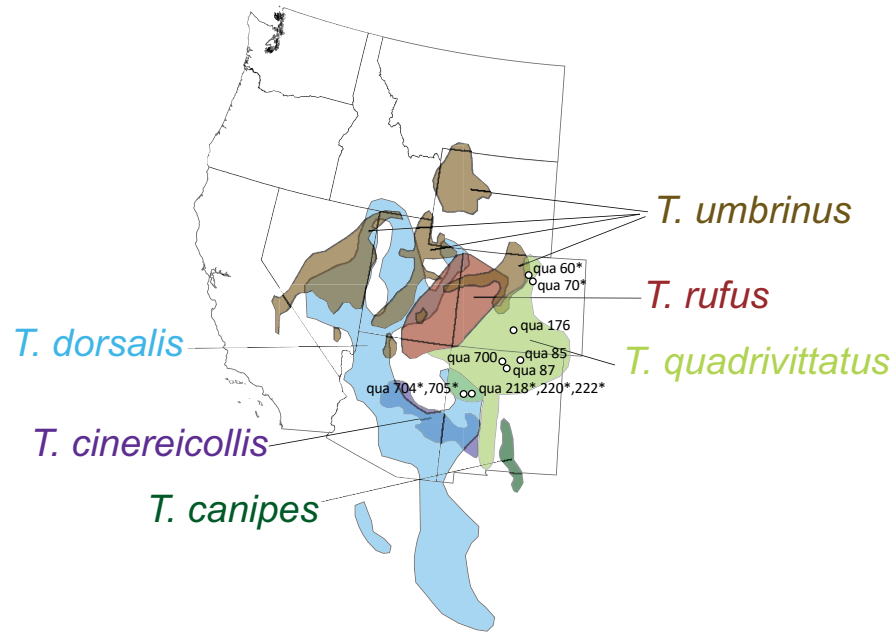


Figure S4. Distribution of *T. quadrivittatus* individuals sequenced here. Georeferenced localities are presented in Table S2. Individuals inferred to have introgressed mtDNA genomes are denoted by asterisks.

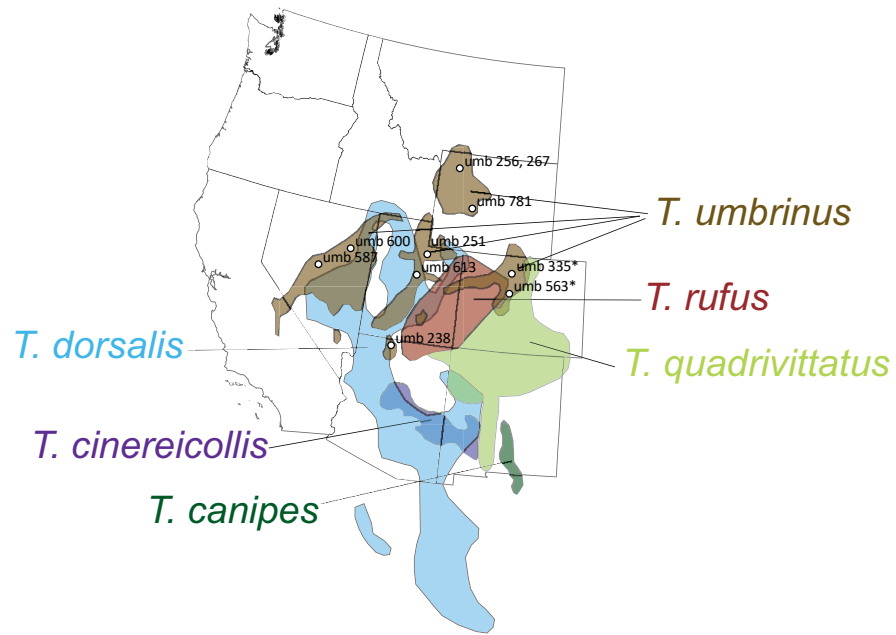


Figure S5. Distribution of *T. umbrinus* individuals sequenced here. Georeferenced localities are presented in Table S2. Individuals inferred to have introgressed mtDNA genomes are denoted by asterisks.

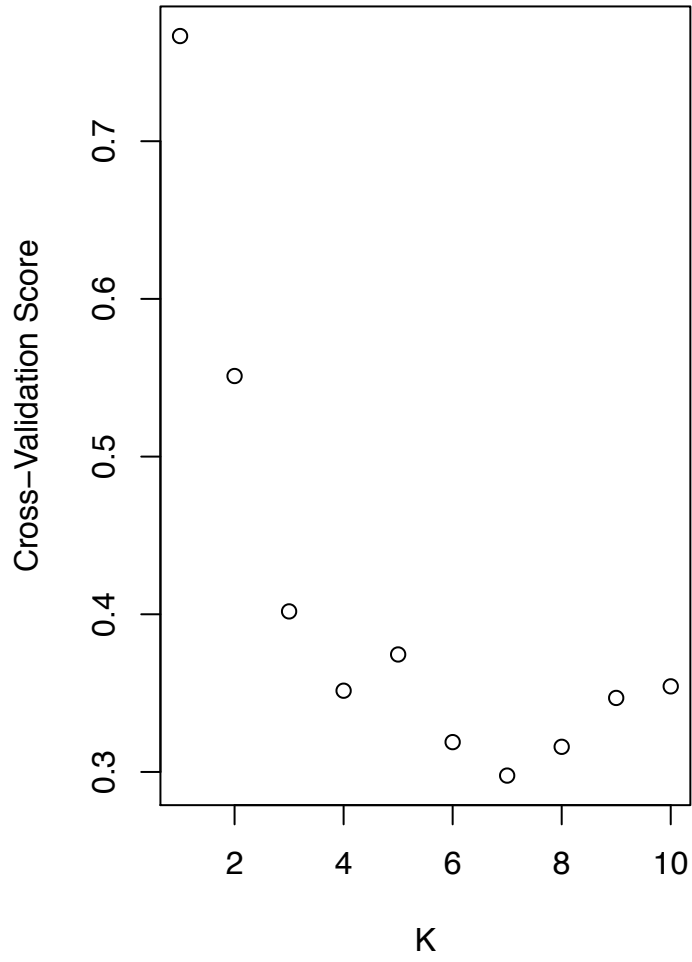


Figure S6. Cross validation of number of populations (K) in ADMIXTURE analyses.

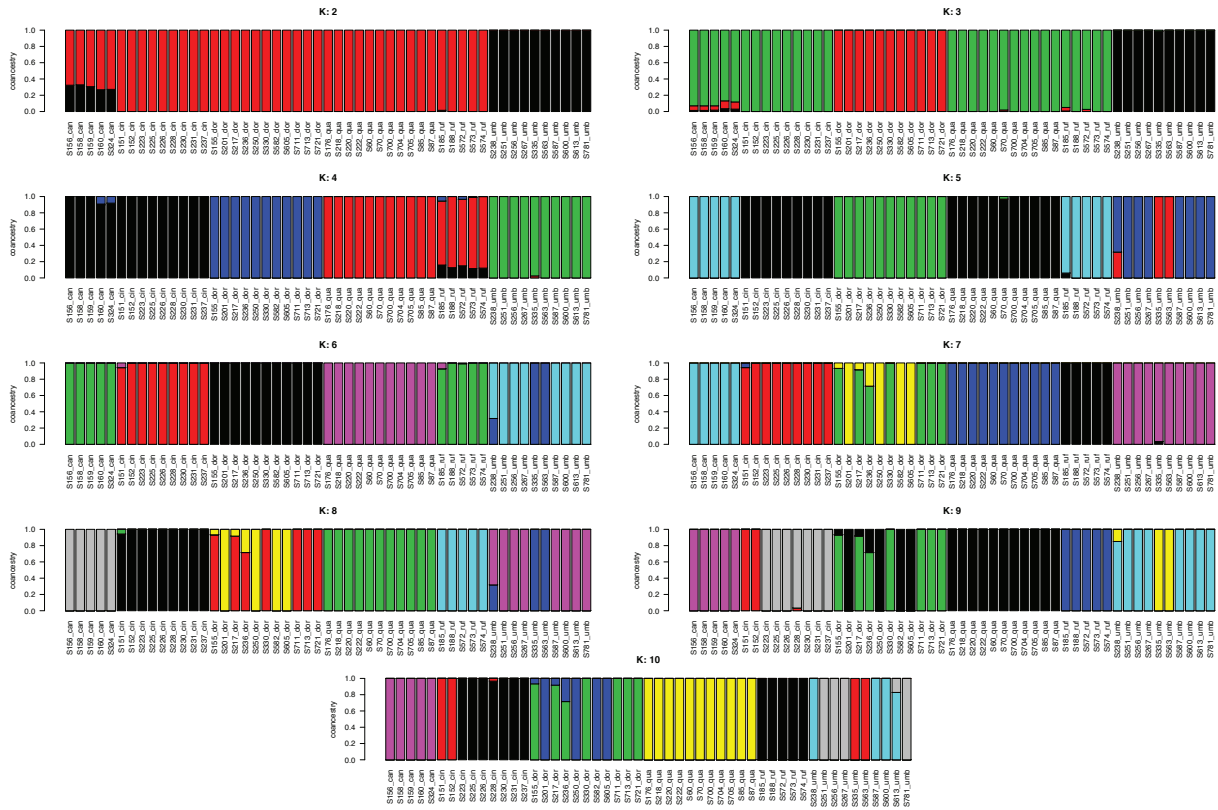


Figure S7. ADMIXTURE results across different values of K.

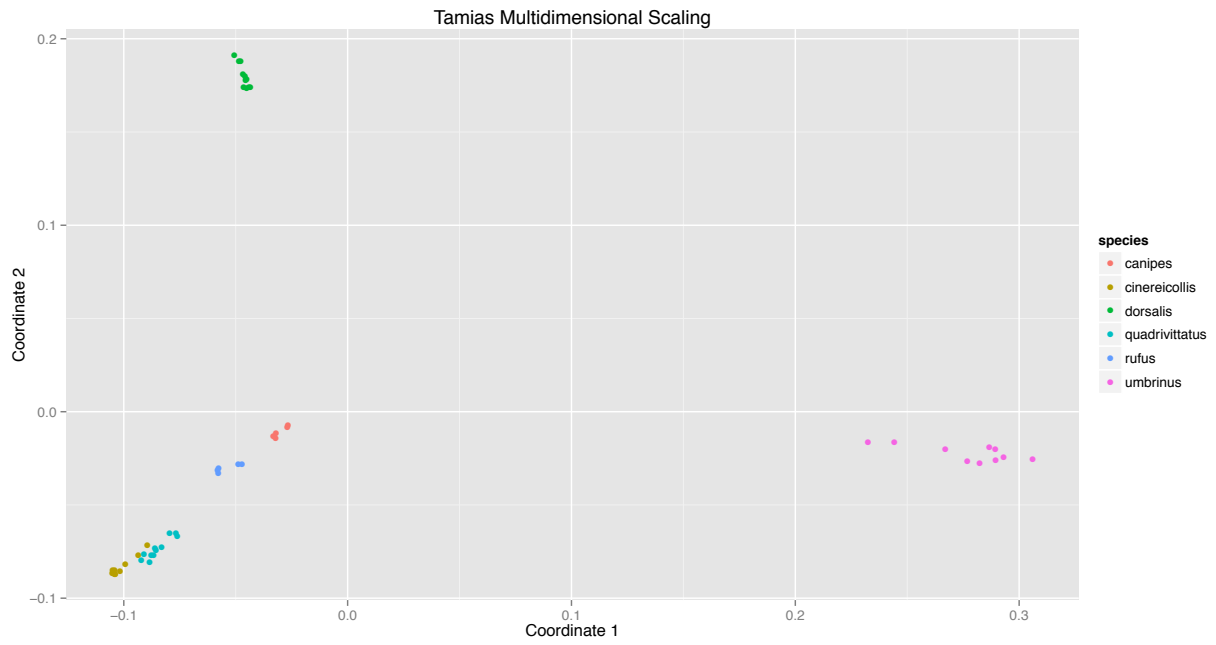


Figure S8. Results of MDS analysis of all genome data generated here.



Figure S9. Results of HyDe analyses for 5 (A-E) sets of quartets. Each quartet includes and outgroup (*T. striatus*), an introgressed *T. dorsalis*, a non-introgressed *T. dorsalis*, and an individual from the species that is the putative source of mtDNA introgression into *T. dorsalis*. On the left of each is the analysis of just nuclear genome data and on the right is the analysis of both nuclear and mtDNA genome data.

